CLAIMS

We claim:

1. A method for characterizing lung tissue in a subject, comprising:

a) providing a lung tissue sample; and

b) detecting a decreased or increased expression relative to a non-cancerous lung tissue control of a marker selected from the group consisting of AOE372, ATP5D, B4GALT, Ppase, GRP58, GSTM4, P4HB, TPI, and UCHL1, thereby characterizing said lung tissue sample.

2. The method of claim 1, wherein said expression is increased at least 4.0 fold relative to said non-cancerous lung tissue control.

3. The method of Claim 1, wherein said detecting the presence of expression of said marker comprises detecting the presence of mRNA corresponding to said marker.

4. The method of Claim 1, wherein said detecting the presence of expression of said marker comprises detecting the presence of a polypeptide corresponding to said marker.

5. The method of Claim 1, wherein said characterizing said lung tissue comprises identifying a stage of lung cancer in said lung tissue.

6. The method of Claim 5, wherein said stage is selected from the group consisting of stage I lung cancer, stage II lung cancer, and stage III lung cancer.

7. The method of Claim 1, further comprising the step of c) providing a prognosis to said subject.

8. A method of characterizing lung cancer, comprising

a) providing a lung cancer tissue sample; and

b) detecting the level of expression relative to a non-cancerous lung tissue control of a marker selected from the group consisting of GRP-58, PSMC, VIM, SOD, TPI, thereby characterizing said lung cancer tissue sample.

9. The method of Claim 8, wherein an increased level of GRP-58, PSMC, and VIM is indicative of stage III lung cancer.

10. The method of Claim 8, wherein a decreased level of SOD and TPI is indicative of stage III lung cancer.

11. A method of predicting survival in lung cancer patients, comprising

a) providing lung cancer tissue sample from a subject;

b) detecting the presence or absence of a marker selected from the group consisting of CK19, CK7, and CK8 in said lung cancer tissue sample.

12. The method of Claim 11, wherein the presence of said marker is indicative of decreased survival of said subject.

13. A lung cancer expression profile map comprising gene expression level information for two or more markers selected from the group consisting of BAG1, CASP4, FADD, P63, 5T4, ITGA2, KRT18, KRT19, KRT7, LAMB1, TMSB4X, TUBA1, BMP2, CDC6, H2AFZ, PDAP1, POLD3, REG1A, S100P, SERPINE1, STX1A, ADM, AKAP12, ARHE, DEFB1, GRB7, INHA, ITK, NACA, STC1, TNFAIP6, VEGF, VLDLR, WNT1, WNT10B, HSPA8, ERBB2, FXYD3, HLA-B, HPCAL1, P2RX5, PEX7, SLC20A1, SLC2A1, VDAC2, ALDH8, ALDOA, ATP2B1, CDS1, CSTB, CTSL, CYP24, FUCA1, FUT3, GAPD, GCNT1, HMBS, KYNU, MLN64, MSH3, MT2A, NME2, NP, PACE, PDE7A, PLGL, PPIF, PTPRCAP, RPC, SC4MOL, SLC1A6, UBC, UGP2, UQCRC2, COPEB, CRK, DBP, GARS, HRB, HSU53209, PRDM2, RELA, RPS26, RPS3, RPS6KB1, SUI1, TIEG, TMF1, B1, FEZ2, HPIP, KIAA0005, KIAA0020, KIAA0084, KIAA0153, KIAA0263, KIAA0317 and MGB1.

14. The lung cancer expression profile map of Claim 13, wherein said map is digital information stored in computer memory.

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